

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2002, 20:52:14 ; Search time 1153.49 Seconds
(without alignments)
12688.233 Million cell updates/sec

Title: US-09-635-521A-1

Perfect score: 1362
Sequence: 1 atgagctaccacagcctccc.....ttcagagacatgaatttga 1362

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_estlun:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estov:*
8: em_estov:*
9: em_hic:*
10: gb_estl:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	508.6	37.3	676	10	BE385990 601276636
2	503.6	37.0	591	10	AI884686 w183407.x
3	502.4	36.9	534	10	BE350014 ht07912.x
4	494.4	36.3	814	10	AL567376
5	479.8	35.2	578	10	AI742092 w938h03.x
6	471.2	34.6	759	11	BE126050 601762888
7	464	34.1	843	11	BE125134
8	429.6	31.5	678	10	AI936826 wp69h10.x
9	413.6	30.4	460	10	AI937602
10	409.2	29.9	690	10	AW149665 x140105.x
11	406.6	29.9	821	11	BG752229 602731372
12	386	28.3	387	10	AI272281 ap23c03.x

13	383	28.1	649	10	AM590950
14	379.8	27.9	645	11	BE432379
15	371.2	27.3	699	10	BE395581
16	367.4	27.0	616	10	AI990500
17	361.6	26.5	696	11	BE439382
18	341.8	25.1	381	10	AA834860
19	336.6	24.7	396	10	AA613995
20	324.8	23.8	433	10	AA417651
21	305.6	22.4	551	11	BE858216
22	304.6	22.4	358	10	AI499630
23	303.6	22.3	598	10	AA173383
24	299.6	22.0	589	10	AI859538
25	294	21.6	540	11	BE939693
26	293	21.5	561	10	AM50789
27	292.6	21.5	537	11	BE594242
28	287.6	21.1	1130	12	AK016817
29	285	20.9	1490	12	AK012406
30	278.6	20.5	537	10	AI018769
31	274.6	20.2	549	10	AM652744
32	273.2	20.1	379	10	AI869176
33	268.6	19.7	527	10	AM338938
34	268.2	19.7	395	13	BH045199
35	265.6	19.5	515	10	AI336858
36	264.8	19.4	520	10	BE480975
37	251.4	18.5	367	10	AA780222
38	250.4	18.4	500	10	AM075598
39	249.4	18.3	640	10	AM148557
40	243	17.8	476	11	BF072978
41	240	17.6	368	11	BE935708
42	240	17.6	424	10	AM437808
43	238	17.5	379	10	AA084248
44	229.6	16.9	480	10	AI423162
45	228.6	16.8	313	10	AI480207

ALIGNMENTS

RESULT 1
BE385990/c 676 bp mRNA EST 21-JUL-2000
LOCUS 601276636F1 NIH_MGC.20 Homo sapiens CDNA clone IMAGE:361766 5',
DEFINITION BE385990
ACCESSION BE385990
VERSION BE385990.1 GI:9331355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCPD/DP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: LINC285 row: g column: 09
High quality sequence stop: 653.
Location/Qualifiers
1. 676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:361766"
/clone_lib="NIH_MGC.20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Skin; Vector: pOT7; Site_1: XhoI; Site_2:

FEATURES

Source
1. 676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:361766"
/clone_lib="NIH_MGC.20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Skin; Vector: pOT7; Site_1: XhoI; Site_2:

EcORI: cDNA made by oligo-dT priming. Directionally
 cloned into EcORI/XhoI sites using the following 5',
 adaptor: GGCACGAG(c). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 168 a 172 c 199 g 137 t
 ORIGIN

Query Match	37.3%	Score 508.6;	DB 10;	Length 676;
Best Local Similarity	99.28;	Pred. No. 2e-101;		
Matches 511; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	848	ttcttcacgaagcctatggtgtgtgacatttgccgtatbctgtgaagcccaacgaatttcgga	907
Db	530	TCtGCCAGGcCTATtTGtTGACATtTGgCCGtGATtGCTGATtGtGCCACACCAATtTCGGA	471
QY	908	ggatcatgtgctgtcgcccaaacccaagcagacttggacagagttcctaattccggggtaca	967
Db	470	GGATCATGgCTGCGCGCCAAACCCAAAGCACAGCTGGAGAGAGtGCTCACTTCtCCGGCGCTTACA	411
QY	968	tgatccctccccccttcctggagaagcttttccactcaagctggtatcatcaaacccgtcc	1022
Db	410	TGATCtTCtCCtCCCTTCtCCGAGACGtTTTtTCACTCAAGTGGtGtCATCAACCCGCTCC	351
QY	1028	tgtacacggtgtccctcgcagcagatttcgcgggtgttcgtgcagatgtgctgtgcgcgc	108
Db	350	TGTACACAGGtGTCTCTCCACACAGtTTTCGGGGGtGTTCGTGCAGGtGTGtGTGCTGCCTGCGCC	291
QY	1088	tgatgcctgcagcagcccaacacagagaaagcgtcgtgcgtacatatgagcaactccacaacg	114
Db	290	TGTGCTGCGAGACAGCCACACAGAGAGAGCGCTGGCGCTACATGCGCACTCCACACACCG	231
QY	1148	acagcgcgcgcttgtgtgcagcccgcttgctcttccttcgagtcctccgcgcagctcctgcga	120
Db	230	ACACGCGCCCTTGTGTGCACAGCGCCGCTTGTCTTCGCTCCCGGCCACAGTCTCTGCAA	171
QY	1208	ggagaacttgaagaagatttcttaagcaactttcaagcagcagcgccgagcccaagctcaagt	126
Db	170	GGAGAACTGGAAGATTTTtTTAAGCACTTTTGAAGCGAGGCGCCGAGCCCAAGTCAAGT	111
QY	1268	cccaagtcattgagttctcagatcactaagagcccaactcagcgcgcagaaaccaagcaattctg	1327
Db	110	CCAGTCAATTGAATCTCGAATCACTAGAGGCCCAACTCAGGCGGGAACACGACCAATTTCG	51
QY	1328	ctgcagaagaatggtttcttcagagacatgaagaatttga	1362
Db	50	CTGACAGAAATGtTTTTCAGACATGAAGtTTTGA	16

RESULT	2
LOCUS	A1884686
DEFINITION	A1884686 591 bp mRNA EST 07-MAR-2000 w183d07.x1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431501 3'
ACCESSION	Similar to SW-GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.
VERSION	A1884686
KEYWORDS	A1884686.1 GI:5589850 EST.
SOURCE	human. Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 591) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index Unpublished (1998)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Ronaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/bdrrp/image/image.html
 Insert Length: 1462 Std Error: 0.00
 Seq primer: -400P from GIDCO
 High quality sequence stop: 444.
 Location/Qualifiers
 1. 591

FEATURES	SOURCE
Location/Qualifiers	1..591
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/db_xref="taxon:9606"	
/clone="IMAGE:2431501"	
/clone_id="NCI_AGAP_Brn25"	
/tissue_type="anaplastic oligodendroglioma"	
/lab_host="DH108"	
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'] TGTTACCAATCTGAAGTGGAGGCGCCGCTATGATTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	109 a 179 c 147 g 155 t 1 others
ORIGIN	

Query Match	37.0%;	Score 503.6;	DB 10;	Length 591;
Best Local Similarity	99.0%;	Pred. No. 2,4e-100;		
Matches 506;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
QY	848	tctctctgaagcctgattgttltgtgacatttggccgtatctgtatgccccaaacagattcgya	907	
Db	80	TCCTCCCAAGGGCGATGTTGTGACATTTGGCCGTATGCTGGATGCCAACACAGATTGCGA	139	
QY	908	ggatcatgagctgcyggyccaaacccaagaacagatctggaagaggttctactattccgggcgtaca	967	
Db	140	GGATCATAGCGCTCGGGCCAAACCCAAAGACAGCTGGAGAGAGGTCTTACTTCGGGGCGTACA	199	
QY	968	tgaatccctcccccctctctcgagagacgtttttctacccctcagctcggtatcaaccgcttc	1027	
Db	200	TGAATCTCTCTCCCTTCTTCGGAGACGTTTTTTTACTCTCACTGCTGGGTATTAACCCGCTCC	259	
QY	1028	tgtaacagctgtctctcgcaacagtttcgycgagtglttcgttcagatgtctgtgtccgc	1087	
Db	260	TGTACACGGTGTCTCTCGACAGATTTCGGCGGGGTTCGTGACAGGTGCTGTGGTGGCC	319	
QY	1088	tgctgcctgcagcaagccaacacgaagaagcgctgtgcgtacatgtgcacatccaacacg	1147	
Db	320	TGTGCTGTCAGACAGCCCAACACAGAGAGGGCCGTGACATATGCGCACTCCACACACCG	379	
QY	1148	acagcgccgccttgtgtcagcgccggtgtgtctcttcgcgtcccgagcgccagttccttcgaa	1207	
Db	380	ACAGCGCCCGCTTTGTGTCAAGCGCCCGCTGTCTTTCCGCTCCGGCGCCAGTCTCTTCGAA	439	
QY	1208	ggaagaactgaaagatttcttaagaaccttltagaagcgagcgccgaaccccaagtltaagt	1267	
Db	440	GGAGAACTGAGAAATTTTCTTAAAGCACTTTTCAGAGCGAGCGCCGACCCACGACTTAAGT	499	
QY	1268	cccaagtcatttgatctctcgaatcaactagagcccaactcgaagcgcgaaacagccaattctg	1327	
Db	500	CCGAGTCATTGAATCTCGAGTCACTAAGGCCAACTCAGCGGAAACCGACCAATTTCTG	559	
QY	1328	ctgcagaagaatgttttcaggaagcatgaagt	1358	
Db	560	CTGCAGAGAAATGCTTTTCANAGACATGAAGT	590	

QY	1028	tgtaacaggtctccctcgcaacaaatttcgaggggttctctgtgaagtgctgtgtctgcgc	1087
Db	266	TGTACAGGTTCTCTCCACAGATTTCGGGGGATGTTCGTGACAGGTGCTGTCTCCGCC	325
QY	1088	tgtagctgcagcaagcccaacacagagaagcgctgtgcgtacatgcgaatccacacagc	1147
Db	326	TGTGGCTGCACACAGCCACACAGAGAAGCGCTGGCGCTACATGCGACTCCACCAACC	385
QY	1148	acagcgcccgcttctgtgcaagcgccgcttgcctctctgcgtcccgcgccagttccttgcaa	1207
Db	386	ACACGCGCCGCTTGTGTGCAGNCGCCGTTGGTCTTGCCTCCGGGGCAGTTCTGTGAA	445
QY	1208	ggagaaactgagaagaattctttaagcaactttcagagcagcgagccagccagttcaagt	1267
Db	446	GGAAACATGGAAGATTTTATTTAAGCACTTTTCAGACGACGGCCGACGCCAGTCTAAGT	505
QY	1268	ccagatattgaagctctcgaagtaactagagcccaactcagcgcgcgaaacacagccaattctg	1327
Db	506	CCCGATTAAATTGAGTCTCGAATTATTATGACCCCAACTCAGGGGNGAAGAACAGCCAAATTCTG	565
QY	1328	ctgcagagaatggttttcagagaaactgaaatttga	1362
Db	566	CTGCAGAGAAATGCTTTCAAGAGACATGAAGTTTGA	600

RESULT	5
LOCUS	AI742092
DEFINITION	AI742092 578 bp mRNA EST 19-DEC-1999
	w938t03.x1 Soares_NSE_F8_9W_OT_PA.P_S1 Homo sapiens CDNA clone

ACCESSION	A1742092
VERSION	A1742092.1
GI	5110380

SOURCE	human
ORGANISM	HOMO

REFERENCE
1 (bases 1 to 578)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS	TITLE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 806 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 460

FEATURES

SOURCE

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2367413"
/clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pRT3p-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer
in a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSP pool 1:
309384-110919, 332082-325895 Soares NBHSP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152337 Soares NB2H8F-9W pool 1:
758280-760583, 772104-774407 Soares NBHFA pool 1:
304776-306511, 320136-322823, 326280-326653 Soares NBHOT
pool 1: 723702-726407, 739080-740999 Subtraction by Bencio

```

Soares and M. Fatima Bonaldo."	
BASE COUNT	
ORIGIN	
102 a	176 c
142 g	158 t

Query Match	35.2%;	Score 479.8;	DB 10;	Length 578;
Best Local Similarity	98.6%;	Pred. No. 4e-95;		
Matches 484;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

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 ||| || |||||
 88 TCCTGCCAGGGCTGATTGTGTGACATTGGCCGTATGCTGGATGCCCAACAGATTGCGA 147

908 ggatcatgctgcgcgccaaccgaacacgactggacgagttcctacttcggggttaca 967

Db 148 GGATCATGGCTGGGCCCCAAACCCAAAGCAGACATGGAGCAGAGTCTCACTTCGCGGCGTACA 207

QY 968 tgatcctcctccccctctctcggagacgtttttctcacctcagctctcgtgtcattcaaccgcctcc 102

DB 208 1GAGCCCTCCCTCCCTCTCTGGAGACGTTTTCTACCCCTGACCTGGCATCACCCGTTCC 267

[illegible][illegible]

Db 328 TGTGCTGCAGCAGCCCAACCAACGAGAGAAGCGCTTGGCGCTTACATGCGGCACCTCACCACC 387

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Db 388 ACACGCCCCGCTTTGTGCA6CGCCCGTTGCTCTTGGCGTCCCGCGGCCAGTCCCTGCAA 447

QY 1208 ggaggaactgagaagatttctctaagcactttcagagcgagggccgagcccaagtctaagt 126

Db 448 GGAGACTGAGAGATTTTCTTAACCACTTTCAGAGCGAGGCCGACCTTAAGT 507

QY 1268 cccgcgtcattgagtcctcgagtcactagagcccaactcagcgcgaaaccagccattctg 1322

Db 508 CCCAGTCATTGAGTCTCGAGTCACCTAGAGCCCACTCAGGGCGCAACACAGCCATTCTG 567

0Y 1338 ctgcagagaat 1338
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 560 cttccctctctctat 570

DD 300 C10CAGAGAI 5/8

RESULT 6
BF126050/C

LOCUS	BF126050	759 bp	mRNA	EST	24-OCT-2000
DEFINITION	601762888F1	NIH_MGC_20	Homo sapiens	cdna clone	IMAGE:4026092.5

mRNA sequence.
 BF126050
 ACCESION
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 103

KEYWORDS
VERSION
SOURCE
human
EST.
BF126050.1
GI:10965090

ORGANISM Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Primates: Hominidae: Homininae: Homo

REFERENCE
Mammalia; Eutheria;
1 (bases 1 to 759)
Primates; Catarrhini; Hominoidea; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
COMMENT

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCPD/DTP
CDNA Library: Developmental Tissue Bank

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 CDNA Library Preparation: Bing Hong/Kuon Laboratory
 DNA Sequencing by: Truete Genomics Inc

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INT at: image.llnwdna.sequencing.org, incyte genomics, inc.

Plate: LLCM855 row: 0 column: 21
High quality sequence stop: 723.

FEATURES	Location/Qualifiers
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1

Query Match 30.4%; Score 413.6; DB 10; Length 460;

Best Local Similarity 93.7%; Pred. No. 1.2e-80;
Matches 431; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 861 gattgtgtacattgagcgtatgtagtgcacacagattcggagatcatgtctgc 920
DB 1 GATTGATGTGACATTTGGCCCTATGCTGATGCCAACACAGATTCTGTGAGATGCTGC 60
QY 921 gggcaaccccaagacagcagcagcagcagcagcagcagcagcagcagcagc 980
DB 61 GGGCAACCCCAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
QY 981 ctctcgagagcgtttcttcaactcagctcgtatcaaacccgctcgtacacggtgtc 1040
DB 121 CTCTCGAGAGCGTTTTCATACCTCAGCTCGGTATCAGACCCGCTCTGTACAGGTC 180
QY 1041 ctgcagcagcgtttcggcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1100
DB 181 CTCGACGCAATATCGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 1101 cgcacacacagacagacagcagcagcagcagcagcagcagcagcagcagcagc 1160
DB 241 CGCACAACACAGAGAGAGCGCTCGCGGTATGCGCAGCTCCACACAGAGCGCGCTA 300
QY 1161 tgtgacagcagcgt 1220
DB 301 TGTGAGCGCGCGGT 360
QY 1221 gatttcttaagcatttcttaagcagcagcagcagcagcagcagcagcagcagc 1280
DB 361 GATTATTATTAACTGACTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
QY 1281 tctcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1320
DB 421 TCCTGAGTCACTAATACCCCACTCATGCGCAACACAGCC 460

RESULT 10

LOCUS AM149665 690 bp mRNA EST 03-NOV-1999
DEFINITION x140h05.x1 NC1-CGAP_Brim50 Homo sapiens cDNA clone IMAGE:2620569.3,
similar to SW:6939_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.; mRNA sequence.

ACCESSION AM149665
VERSION AM149665.1 GI:6197561
KEYWORDS EST.

SOURCE

ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 690)
NC1/NIHDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
(CGAP/BTGA), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NC1-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/dbirp/image/image.html

JOURNAL COMMENT

Journal Comment
Possible reversed clone: similarity on wrong strand
Seq primer: 400p from Gibco
High quality sequence stop: 402.
Location/Qualifiers
1..690

FEATURES

Source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2620569"
/clone_lib="NC1-CGAP_Brim50"
/tissue_type="medulloblastoma"
/lab_host="DH10B (phage resistant)"
/note="Organ: brain; Vector: pTZ19-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from a
medulloblastoma tumor tissue, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTZ19 vector. This library is normalized. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

142 a 196 c 160 g 191 t 1 others

Query Match 30.0%; Score 409.2; DB 10; Length 690;

Best Local Similarity 95.7%; Pred. No. 1.2e-79;
Matches 420; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 848 tcttctgagcgtgattgt 907
DB 251 TGTGCCAGGCGCTGATGT 310
QY 908 ggtatctgt 967
DB 311 GGATCATGCTGCGGCGCAACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 370
QY 968 tgaatctctcctcctctcctcctcctcctcctcctcctcctcctcctcctcctc 1027
DB 371 TGATCCCTCCCTCCCTCTCTGAGACGTTTTCATCTCAGCTCGTCATCAACCCCTCC 430
QY 1028 tgaacagcgt 1087
DB 431 TGTAACAGGCTGTCTCTGACAGCTTTCGCGGGGTGTGTGTGTGTGTGTGTGTGTGT 490
QY 1088 tgtcgt 1147
DB 491 TGTGCTGTGACAGCGCCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 550
QY 1148 acagcgcgccttctgt 1207
DB 551 ACAGCGCGCGCTTGT 610
QY 1208 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1267
DB 611 GGAGAACTGAGAAATTTCTTAAACCTTCAAGAACGAGCCGACCCCAAGCTTAAT 670
QY 1268 ccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1286
DB 671 TCAGTCACTGATTTTGA 689

RESULT 11

LOCUS BG752229 821 bp mRNA EST 15-MAY-2001
DEFINITION 602731372F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875113.5,
mRNA sequence.

ACCESSION BG752229
VERSION BG752229.1 GI:14062882
KEYWORDS EST.
SOURCE human.
ORGANISM human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 821)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

JOURNAL COMMENT
Possible reversed clone: similarity on wrong strand
Seq primer: 400p from Gibco
High quality sequence stop: 402.
Location/Qualifiers
1..690

Accession	Sequence	Position
Db	TCGACGAGATTTCGGCGGGGTGTTCGTGGAGGTGCTGTCTGCGCTTCGCTGGAGCAC	148
Qy	gccaaccaaggaagcgactgcggtacatcgtcactccaccaaccgacagcgccgcttt	1161
Db	GCCAAACCGAGAAAGCGCCTGCGCGTACATCGCGACTCCACACGAGACGAGCGCCGCTT	88
Qy	gttagagcgccgcttgctcttcgcgtcccgcgcgcccaagtcctctcgaaggaagactgagaag	1221
Db	GTGACGCCCCGCTGCTCTTGGCGTCCGCGGCCAGTCTCTGCAGAGGAACATGAGAAG	28
Qy	attctcctaagcacttttcagaagcgag	1248
Db	ATTTCCTTAACCACTTTTCAGAGCGAG	1

RESULT	13
AM590950	
LOCUS	AM590950
DEFINITION	h51e12.x1 NCI_CGAP-Gc6 Homo sapiens cDNA clone IMAGE:2949166 3'
ACCESSION	similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39.; mRNA sequence.
VERSION	AM590950
KEYWORDS	AM590950.1 GI:7278094
SOURCE	EST.
ORGANISM	human.
DATE	22-MAR-2000

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 649)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg Ph.D.

JOURNAL COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/INTL at: [Image.llnl.gov/image/html/resources.shtml](http://image.llnl.gov/image/html/resources.shtml)

Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 457.

RES
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2949166"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10b"
/notice="Vector: pT73d-Pac (Pharmacia) with a modified
polylinker: Site.1: Not I; Site.2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
55 circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonings
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

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Query Match	28.1%;	Score 383;	DB 10;	Length 649;
Best Local Similarity	97.3%;	Pred. No. 6.6e-74;		
Matches 400; Conservative	0;	Mismatches 10;	Indels 1;	Gaps 1

QY 848 tcttctcgaagccgatgtttgttgaacttgcgcgtatgtcttgatgcccacaagaatttcga 907

Db 240 TCTGCCAGGGGCTGATGTTGTTGTACATTGTGGCGTATGCTGCATGCCCAACCAAGATTGGCA 299

QY 908 ggaatcatgagctgcgcgcacaacccaagaacgaacttgagacgaggttctacttcgcggcgtaca 967

Db 300 GGATCATGAGTGTGCGGCCAACAACCAAGCAGACTGAGCAGAGGTCTACTTCGGGCGTACA 359

QY 968 tgatctctctccccctctctcggagaagttttctactaagctcgtgtacaaccgcgtcc 1027

Db 360 TGATCTCCCTCCCTTCTCTCGAGAGCTTTTCTACCTCAGCTCGGTCATCAACCCGCTCC 419

QY 1028 tgtaacagatgactcctcgcagcagatttcggcggagtttctgtgaagtgtctgtgcgcgc 1087

Db 420 TGTACACGGTGTCTCTGCAACAGTTTCGGCGGGTGTTCGTCAAGTCTGTGCTGCGCGCC 479

QY 1088 tgctgcgtcagcagcgcacaaccacagaaagcgcgtcgcgtacagcgcgaacttccacaacacg 1147

Db 480 TGTGCGTGGACGACGCCCAACAGAGAAGCGCGTACGCGGTACATGCGGCACCTCCACACCG 539

QY 1148 acagagccgcgttctgtgaagagcccggttgctcttcgcgtccgcgcgcagatcctctgcaa 1207

Db 540 ACAGCGCGCCCTTTGTGACGCGCCCGTTGATCTTCGTACCGCGCGCAAGTCTCCTGTGCAA 599

QY 1208 ggaagaactgagaagaatttcttaaacacttttcgaagagagagagcggaacccc 1258

Db 600 GGAAGAATCGAAGAATTGTTTAAACAC-ATTCAAGAGGAAGCGGACCGCC 649

RESULT	14
BF432379	
LOCUS	BF432379 645 bp mRNA
DEFINITION	nm033511.x1 NCI-CCG4-BR23 Homo sapiens cDNA clone IMAGE:3406292 3'
	similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
	GP39. ; mRNA sequence.
ACCESSION	BF432379
VERSION	BF432379.1 GI:11444509
KEYWORDS	EST.
SOURCE	human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 645)
NCBI/NCINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: inf@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 441.
Location/Qualifiers
I. .645

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1="IMAGE:3406292"
/clone_1_id="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
/notes="Organ: brain; Vector: pRTT3-Pac (Pharmacia) with a
strand polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAAGTGGAGGCGCCGATATCTTTTTTTTTTTTTTTTTT

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Wed Jan 9 08:51:39 2002

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